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BY: Helene Gabel Date: March 9, 2006

**IN THE UNITED STATES PATENT AND TRADEMARK OFFICE**

First Named Inventor:	Nobuya ITOH	§	Group Art Unit: 1652
		§	
		§	
Conf. No.:	7835	§	Examiner: Kagnew H. Gebreyesus, Ph.D.
		§	
Appln. No.:	10/782,998	§	Allowed December 22, 2005
		§	
Filing Date:	February 20, 2004	§	Attorney Docket No.: 600630-15US
		§	(562737)
Title:	REDUCTASE GENE AND USE OF THE SAME		

**DECLARATION OF NOBUYA ITOH**  
**REGARDING REPLACEMENT SEQUENCE LISTINGS**

I, Nobuya Itoh, hereby declare as follows:

1. I am the inventor and applicant in the above-identified patent application.

2. Upon reviewing the Notice of Allowance dated December 22, 2005, concerning this application. I realized that corrections to the Sequence Listings for SEQ ID NOS:1 and 2 which had been identified earlier had never been made during the prosecution of this application. I realized that there were errors when I started another study about the gene of the present invention and analyzed the nucleotide sequences in the same way repeatedly, thereby noticing some mistakes in the sequences.

3. The errors occurred as a result of simple mistakes when analyzing the nucleotide sequence of SEQ ID NO:2 with an ABI Prism 310 Genetic Analyzer, where the mistakes are identified as follows:

1. 123<sup>rd</sup> Nucleotide: Peak of "C" was buried by peak "A" due to succession of "A".
2. 246<sup>th</sup> Nucleotide: Peak of "A" was confirmed by performing analysis again.

3. 467<sup>th</sup> Nucleotide: Peak of "C" was buried by peak "G" due to continuation of "G" and "C".
4. 593<sup>rd</sup> Nucleotide: Peak of "C" was buried due to succession of "T" and "C" and low sensitivity of peak "C".
5. 595<sup>th</sup> Nucleotide: Peak of "C" was buried due to succession of "T" and "C" and low sensitivity of peak "C".
6. 617<sup>th</sup> Nucleotide: Peak of "C" was buried by peak "T" due to continuation of "T" and "C".
7. 620<sup>th</sup> Nucleotide: Peak of "G" was buried due to succession of "A" and "G" and low sensitivity of peak "G".
8. 692<sup>nd</sup> Nucleotide: Peak of "G" was confirmed by performing analysis again.

4. Attached is a copy of a ClustalW Formatted Alignments printout showing the eight mistakes identified in paragraph 3 above. Also attached is a comparison of the original and amended nucleotide sequence for SEQ ID NO:2.

5. The errors were inadvertent and without any disceptive intention.

6. Since the DNA of SEQ ID NO:2 is from the same *Leifsonia* sp. S-749 (Accession No. of International Depositary Authority: FERM BP-8291) as set forth in the application, no new matter has been added by correcting the nucleotide sequence of the DNA in SEQ ID NO:2.

7. In view of the corrections made to SEQ ID NO:2, the corresponding amino acids of SEQ ID NO:1 coded by the DNA of SEQ ID NO:2 also required correction. The corrections are noted in the attached comparison of the original amino acid sequence and the amended amino acid sequence for SEQ ID NO:1. For the same reasons as mentioned in paragraph 6, although corrections have been made to the amino acid sequence, no new matter has been added.

I hereby declare that all statements made herein of my own knowledge are true and that all statements made on information and belief are believed to be true; and further, that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under Section 1001 of Title 18 of the United States

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Code and that such willful false statements may jeopardize the validity of the application or any patent issuing thereon.

NOBUYA ITOH

March 9, 2006  
(Date)

Nobuya Itoh

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SEQ ID NO: 2

## Original nucleotide sequence

## Amended nucleotide sequence

10	20	30	40	50	60	10	20	30	40	50	60
atggtcagtcacgacgctgcgcgacccggttcgcgcatcgtgacccgaggcgctcgggcac						atggtcagtcacgacgctgcgcgacccggttcgcgcatcgtgacccgaggcgctcgggcac					
70	80	90	100	110	120	70	80	90	100	110	120
ggggcgccgctggcgctcaactctcgcgcgagcggcgagcgcgctcctcgtcaaccgacctg						ggggcgccgctggcgctcaactctcgcgcgagcggcgagcgcgctcctcgtcaaccgacctg					
130	140	150	160	170	180	130	140	150	160	170	180
aaagaggagcagcgcgagccgctcgtggccgagatcgagccgcggttaaggccgc						aaagaggagcagcgcgagccgctcgtggccgagatcgagccgcggttaaggccgc					
190	200	210	220	230	240	190	200	210	220	230	240
gcgctcggggcgagcgtgacgcgaccccggttcggcgagcggcgagcgtcgcggggcggaac						gcgctcggggcgagcgtgacgcgaccccggttcggcgagcggcgagcgtcgcggggcggaac					
250	260	270	280	290	300	250	260	270	280	290	300
gcttcggggccctcaagtcggtcaaacgcgggcatcggcgagcggcgagccgcacg						gcttcggggccctcaagtcggtcaaacgcgggcatcggcgagcggcgagccgcacg					
310	320	330	340	350	360	310	320	330	340	350	360
gtcggcgactactcgtcgacagctggcgacagtgatcgagggtcaacctcaacgcctg						gtcggcgactactcgtcgacagctggcgacagtgatcgagggtcaacctcaacgcctg					
370	380	390	400	410	420	370	380	390	400	410	420
ttctacgggatgcagcgcgacgtgaagccatggccgcgaacggcggtgcgctcgtc						ttctacgggatgcagcgcgacgtgaagccatggccgcgaacggcggtgcgctcgtc					
430	440	450	460	470	480	430	440	450	460	470	480
aacatgggtccatcctgggaagcgtcggttcgcgcaactcgtcgggtaacgtcacggcc						aacatgggtccatcctgggaagcgtcggttcgcgcaactcgtcgggtaacgtcacggcc					
490	500	510	520	530	540	490	500	510	520	530	540
aagcacgcgtgctcgtcaccagaaacgcgcgctcgagtagcgcgcgcgacaaaggtg						aagcacgcgtgctcgtcaccagaaacgcgcgctcgagtagcgcgcgcgacaaaggtg					
550	560	570	580	590	600	550	560	570	580	590	600
cgcgtcgtcgcgtcgcccggttcctccgcgacccgctcgtggaggaacattctcgg						cgcgtcgtcgcgtcgcccggttcctccgcgacccgctcgtggaggaacattctcgg					
610	620	630	640	650	660	610	620	630	640	650	660
cgacgcgtggcgttcctaaaggaagcacgcgcctcgccgctgggcgagcgcggaagag						cgacgcgtggcgttcctaaaggaagcacgcgcctcgccgctgggcgagcgcggaagag					
670	680	690	700	710	720	670	680	690	700	710	720
gtcgcctcgtggtcgcgttcctcgcctcgcgacgcgcgagcttcacaccggcagctac						gtcgcctcgtggtcgcgttcctcgcctcgcgacgcgcgagcttcacaccggcagctac					
730	740	750				730	740	750			
cacctggtagcggcggtacaccgccagtg						cacctggtagcggcggtacaccgccagtg					

SEQ ID NO: 1

## Original amino acid sequence

10 MetAlaGlnTyrAspValAlaAAspArgSerAlaIleValThrGlyGlySerGlyIle 20  
30 GlyArgAlaValAlaLeuThrLeuAlaAAspSerGlyAlaAValLeuValThrAspLeu 40  
50 LysGluGluHisAlaGlnAlaValValAlaGluIleGluAlaAAGlyGlyLysAlaAla 60  
70 AlaLeuAlaGlyAspValThrAspProAlaPheGlyGluAlaSerValAlaGlyAlaAsn 80  
90 AlaLeuAlaProLeuLysIleAlaValAsnAlaGlyIleGlyGlyGluAlaAlaThr 100  
110 ValGlyAspTyrSerLeuAspSerTrpArgThrValIleGluValAsnLeuAlaVal 120  
130 PheTyrGlyMetGlnProGlnLeuLysAlaMetAlaAAspGlyGlyAlaIleVal 140  
150 AsnMetAlaSerIleLeuGlySerValGlyPheAlaAsnSerSerGlyTyrValThrAla 160  
170 LysHisAlaLeuGlyLeuThrGlnAsnAlaAlaLeuGluTyrAlaAAspLysVal 180  
190 ArgValValAlaValGlyProGlyPheIleArgThrArgSerTrpArgGlnLeuPheArg 200  
210 ArgArgAlaGlyValLeuGlnGlyLysHisAlaLeuGlyArgLeuGlyGluProGluGlu 220  
230 ValAlaSerLeuValAlaPheLeuAlaSerAspAlaAlaSerPheIleThrGlySerTyr 240  
250 HisLeuValAspGlyGlyTyrThrAlaGln

41 Lys ⇒ Asn

156 Gly ⇒ Ala

198 Leu ⇒ Pro

199 Phe ⇒ Leu

206 Leu ⇒ Pro

207 Gln ⇒ Arg

231 Asp ⇒ Gly

## Amended amino acid sequence

10 MetAlaGlnTyrAspValAlaAAspArgSerAlaIleValThrGlyGlySerGlyIle 20  
30 GlyArgAlaValAlaLeuThrLeuAlaAAspSerGlyAlaAValLeuValThrAspLeu 40  
50 AsnGluGluHisAlaGlnAlaValValAlaGluIleGluAlaAAGlyGlyLysAlaAla 60  
70 AlaLeuAlaGlyAspValThrAspProAlaPheGlyGluAlaSerValAlaGlyAlaAsn 80  
90 AlaLeuAlaProLeuLysIleAlaValAsnAlaGlyIleGlyGlyGluAlaAlaThr 100  
110 ValGlyAspTyrSerLeuAspSerTrpArgThrValIleGluValAsnLeuAlaVal 120  
130 PheTyrGlyMetGlnProGlnLeuLysAlaMetAlaAAspGlyGlyAlaIleVal 140  
150 AsnMetAlaSerIleLeuGlySerValGlyPheAlaAsnSerSerAlaTyrValThrAla 160  
170 LysHisAlaLeuGlyLeuThrGlnAsnAlaAlaLeuGluTyrAlaAAspLysVal 180  
190 ArgValValAlaValGlyProGlyPheIleArgThrArgSerTrpArgGlnProLeuArg 200  
210 ArgArgAlaGlyValProArgGlyLysHisAlaLeuGlyArgLeuGlyGluProGluGlu 220  
230 ValAlaSerLeuValAlaPheLeuAlaSerGlyAlaAlaSerPheIleThrGlySerTyr 240  
250 HisLeuValAspGlyGlyTyrThrAlaGln